SEQUENCE LISTING (A)

<110> Forschungszentrum Juelich GmbH; Marina Vrlijc et al

<120> Process for the microbial production of amino acids by

boosted activity of export carriers

<130> 1

<140> PCT/DE96/02485

<141> 1996-12-18

<160> 2

<170> PatentIn Ver. 2.0

<210> 1

<211> 2374

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS lysE (Lysin-Exporter)

<222> (1016)..(1726)

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gtctgtgagt ctagctagag atctagattc caggcgccat cgttgccaat acatcggtgt 180

gtcaatgggt atctcatcga ggaggatcac ttctcctgct tttagcatgg gagcagcttg 240

ggtttcggga agaagtcccc aaccaaggcc tcggcgaatt gcctcaccaa aaccttccgc 300

cgacgggaca atggatacgc gcctgcgccc cacaggacca tcgacgcgcc cgtccaggtc 360

acggtcttga agcacatctt tgggaccgaa gcgtaagacg ggcatcgcag cccaatctag 420

tttcccatca accatgtagg catcccgcaa tgagggggtt gcaatggcca agtggcgcat 480

ggttccaagt tctactactt cacatcccgc cacgggatta gcttcacggg ttaccgctcc 540

taaaacatct ccacgccgca gcaaggataa tgtgtgcgct tcatcttcca agcgcagcgt 600

gagcgttgct ccaccccaag aagctacctc gttgaacacg ggaggaaacc atgtggatag 660

cgaatctgcg ttgatggcga tggttaacgg gatttcagca aggcgtccag atagttgcgc 720

tttagtttct gcttgcagca acaccatttt ccgcgctgct tgcacaagga cttcacccgc 780

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agctttaacg cgctgactca ccgccgaggg ggaaatggaa agggctaagg aggcgccttc 900

gaagctgcct tcatcaatga ttgagagcaa agtgtccagt tgaatggggt tcatgaagct 960

atattaaacc atgttaagaa ccaatcattt tacttaagta cttccatagg tcacg atg   1018

                                                                   Met

                                                                    1

gtg atc atg gaa atc ttc att aca ggt ctg ctt ttg ggg gcc agt ctt   1066

Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu

              5   10   15

tta ctg tcc atc gga ccg cag aat gta ctg gtg att aaa caa gga att   1114

Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile

               20   25   30

aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct gac   1162

Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp

           35   40   45

gtc ttt ttg ttc atc gcc ggc acc ttg ggc gtt gat ctt ttg tcc aat   1210

Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn

  50   55   60   65

gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt ggc atc gct tac   1258

Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr

                 70   75   80

ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac aag   1306

Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys

                 85   90   95

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gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc gat      1354
Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp
        100                 105                 110


gac acg cct ttg ggc ggt tcg gcg gtg gcc act gac acg cgc aac cgg      1402
Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg
        115                 120                 125


gtg cgg gtg gag gtg agc gtc gat aag cag cgg gtt tgg gta aag ccc      1450
Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro
130                 135                 140                 145


atg ttg atg gca atc gtg ctg acc tgg ttg aac ccg aat gcg tat ttg      1498
Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu
            150                 155                 160


gac gcg ttt gtg ttt atc ggc ggc gtc ggc gcg caa tac ggc gac acc      1546
Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr
                165                 170                 175


gga cgg tgg att ttc gcc gct ggc gcg ttc gcg gca agc ctg atc tgg      1594
Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp
            180                 185                 190


ttc ccg ctg gtg ggt ttc ggc gca gca gca ttg tca cgc ccg ctg tcc      1642
Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser
        195                 200                 205
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agc ccc aag gtg tgg cgc tgg atc aac gtc gtc gtg gca gtt gtg atg    1690
Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met
210             215             220             225


acc gca ttg gcc atc aaa ctg atg ttg atg ggt tag tttcgcggg         1736
Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
            230             235



ttttggaatc ggtggccttc gcccaaatgt tgatgccggc gtcgtgggaa atctcatcga 1796


tcgcctccaa ctcggcgtca gaaaactcca agttgttgag tgaatcaagg ctgttgtcca 1856


gctgctcaac tgacgaagca ccaatcaatg cactggtcac ggtatccgcg ccgtactctc 1916


cttgctcgcg cagcacccat gcaagcgcca tctgcgcaag tgactgcccg cgttcctggg 1976


cgatgtcatt gagcttgcgg accatatcaa tattgttcac gttcaacatg ccctcagaca 2036


gggacttacc ctggctggcg cgggaaccct ctggaattcc atcgagatat ttgtccgtga 2096


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gcaacaagtt ctcaccgtca tcgcccggtt cctccaccca acgattaatg atggaatagc 2216


ttggctgatg aatcagaagc gggcagccct cctccgccat gaactcagcc gcctccgctg 2276


tgagctctgg accgtaggaa gaaataccca cgtaaagagc ctttccagac gcaacaatgt 2336


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<212> PRT LysE (Lysin-Exporter)

<213> Corynebacterium glutamicum

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Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
                20   25   30

Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
            35   40   45

Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
        50   55   60

Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
65   70   75   80

Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
                85   90   95

Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro
                100   105   110

Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn
          115   120   125

Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys
          130   135   140

Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr
145   150   155   160

Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp
               165   170   175

Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile
          180   185   190

Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu
          195   200   205

Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val
     210   215   220

Met Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
225   230   235

SEQUENCE LISTING (B)

<110> Forschungszentrum Juelich GmbH; Marina Vrlijc et al.

<120> Process for the microbial production of amino acids by

boosted activity of export carriers

<130> 1

<140> PCT/DE96/02485

<141> 1996-12-18

<160> 3

<170> PatentIn Ver. 2.0

<210> 1

<211> 2374

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS ORF3 (partial)

<222> (2)..(652)

<220>

<221> CDS LysG (Regulator lysE)

<222> (1421)..(2293)

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tct gga aag gct ctt tac gtg ggt att tct tcc tac ggt cca gag ctc 97

Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu

           20   25   30

aca gcg gag gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg 145

Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu

      35   40   45

att cat cag cca agc tat tcc atc att aat cgt tgg gtg gag gaa ccg 193

Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro

  50   55   60

ggc gat gac ggt gag aac ttg ttg cag tca gct gcc aac aat ggt ctt 241

Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu

65   70   75   80

ggc gtc att gct ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa 289

Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys

           85   90   95

tat ctc gat gga att cca gag ggt tcc cgc gcc agc cag ggt aag tcc 337

Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser

           100   105   110

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ctg tct gag ggc atg ttg aac gtg aac aat att gat atg gtc cgc aag      385
Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys
         115                 120                 125


ctc aat gac atc gcc cag gaa cgc ggg cag tca ctt gcg cag atg gcg      433
Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala
         130                 135                 140


ctt gca tgg gtg ctg cgc gag caa gga gag tac ggc gcg gat acc gtg      481
Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val
145                 150                 155                 160


acc agt gca ttg att ggt gct tcg tca gtt gag cag ctg gac aac agc      529
Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser
                 165                 170                 175


ctt gat tca ctc aac aac ttg gag ttt tct gac gcc gag ttg gag gcg      577
Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala
         180                 185                 190


atc gat gag att tcc cac gac gcc ggc atc aac att tgg gcg aag gcc      625
Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala
         195                 200                 205


acc gat tcc aaa acc cgc gaa aac taa cccatcaaca tcagtttgat            672
Thr Asp Ser Lys Thr Arg Glu Asn
         210                 215
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ggacagcggg cgtgacaatg ctgctgcgcc gaaacccacc agcgggaacc agatcaggct 792

tgccgcgaac gcgccagcgg cgaaaatcca ccgtccggtg tcgccgtatt gcgcgccgac 852

gccgccgata aacacaaacg cgtccaaata cgcattcggg ttcaaccagg tcagcacgat 912

tgccatcaac atgggctttTa cccaaacccg ctgcttatcg acgctcacct ccacccgcac 972

ccggttgcgc gtgtcagtgg ccaccgccga accgcccaaa ggcgtgtcat cgggcacggt 1032

tggttctgtt tcttcaatga tctgtggcgc ttccaccttg tttgtcatgg cgtctttcgc 1092

tgccatgacg gcaaaccata acaggtaagc gatgccaccc cagcgcataa tatcgagcac 1152

gatcggcgcg gcattggaca aaagatcaac gcccaggtg ccggcgatga acaaaaagac 1212

gtcagaaatt aaacacacga gaagaaccgc aatgagtcct tcgcgcttaa ttccttgttt 1272

aatcaccagt acattctgcg gtccgatgga cagtaaaaga ctggccccca aaagcagacc 1332

tgtaatgaag atttccatga tcaccatcgt gacctatgga agtacttaag taaaatgatt 1392

ggttcttaac atggtttaat atagcttc atg aac ccc att caa ctg gac act   1444
                                Met Asn Pro Ile Gln Leu Asp Thr
                                         220   225

ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc tcc tta gcc   1492
Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala Ser Leu Ala
            230   235   240

ctt tcc att tcc ccc tcg gcg gtg agt cag cgc gtt aaa gct ctc gag   1540
Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys Ala Leu Glu
            245   250   255

cat cac gtg ggt cga gtg ttg gta tcg cgc acc caa ccg gcc aaa gca   1588
His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro Ala Lys Ala
            260   265   270

acc gaa gcg ggt gaa gtc ctt gtg caa gca gcg cgg aaa atg gtg ttg   1636
Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys Met Val Leu
       275   280   285

ctg caa gca gaa act aaa gcg caa cta tct gga cgc ctt gct gaa atc   1684
Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu Ala Glu Ile
290   295   300   305

ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca tgg ttt cct   1732
Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr Trp Phe Pro
            310   315   320

ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg ctc acg ctg   1780
Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr Leu Thr Leu
            325   330   335

cgc ttg gaa gat gaa gcg cac aca tta tcc ttg ctg cgg cgt gga gat   1828

Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg Arg Gly Asp
      340   345   350

gtt tta gga gcg gta acc cgt gaa gct aat ccc gtg gcg gga tgt gaa   1876
Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala Gly Cys Glu
      355   360   365

gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca acc ccc tca   1924
Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala Thr Pro Ser
370   375   380   385

ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg gct gcg atg   1972
Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp Ala Ala Met
            390   395   400

ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac cgt gac ctg   2020
Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp Arg Asp Leu
            405   410   415

gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta tcc att gtc   2068
Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val Ser Ile Val
            420   425   430

ccg tcg gcg gaa ggt ttt ggt gag gca att cgc cga ggc ctt ggt tgg   2116
Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly Leu Gly Trp
      435   440   445

gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa gca gga gaa   2164

Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys Ala Gly Glu

450   455   460   465

gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg tat tgg caa   2212
Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met Tyr Trp Gln
                470   475   480

cga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca gac gcc gtc   2260
Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr Asp Ala Val
            485   490   495

gtt gat gca gca atc gag gga ttg cgg cct tag ttacttctga aaaggttcag 2313
Val Asp Ala Ala Ile Glu Gly Leu Arg Pro
        500   505

ggttttttcac ttcttcgccc gcaggaattg ggccaggcag agtaacacct tcagcaaatg 2373

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<212> PRT ORF3 (partial)

<213> Corynebacterium glutamicum

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          20   25   30

Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu
          35   40   45

Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro
     50   55   60

Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu
65   70   75   80

Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys
                    85   90   95

Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser
               100   105   110

Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys
          115   120   125

Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala
     130   135   140

Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val
145   150   155   160

Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser

Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala

          180   185   190

Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala

          195   200   205

Thr Asp Ser Lys Thr Arg Glu Asn

       210   215

<210> 3

<211> 290

<212> PRT LysG (Regulator lysE)

<213> Corynebacterium glutamicum

<400> 3

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          20   25   30

Ser Gln Arg Val Lys Ala Leu Glu His His Val Gly Arg Val Leu Val

          35   40   45

Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val

       50   55   60

Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln

65   70   75   80

Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala

               85   90   95

Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser

               100   105   110

Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr

          115   120   125

Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu

     130   135   140

Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg

145   150   155   160

His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp

               165   170   175

Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys

          180   185   190

Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val

     195   200   205

Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu

    210   215   220

Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala

225   230   235   240

Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro

            245   250   255

Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser

            260   265   270

Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu

            275   280   285

Arg Pro

    290